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Effect of cropping systems, mineral nitrogen (N) and crop residue on total soil microbial community under soybean in Meru south (Chuka) central highlands in Kenya

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In Kenya soybean is grown under different soil management systems. Scarce information is found on the effect of cropping systems, N and crop residue application on the diversity of total soil microbial communities. The objective of this study was to evaluate the response of total soil microbial communities to different soybean cropping systems, N and crop residue incorporation. Four cropping systems each per main plot were compared; mono-legume (ML), mono-cereal (MC), association (AS) and rotation (RO). N and crop residue were randomly applied in a split pattern. Soil samples were collected at (0-10 cm) depth from each sub-plot after three years and at time zero for comparison. Soil microbial DNA was analyzed using Polymerase Chain Reaction–Denaturing Gradient Gel Electrophoresis method based on 16S/18S rDNA to assess the composition of both bacterial and fungal communities.

After 3 years, diversity of total bacterial communities after cropping was significantly lower compared to diversity at time zero. AS plots had significantly lower diversity of total bacterial communities compared to the other cropping systems. Crop residue applications had no significant effect on diversity of total bacterial communities. On the other hand, plots having received crop residues had significantly higher diversity of total fungal communities compared to those which did not receive crop residues. Additionally, diversity of total fungal communities was significantly lower under MC and ML systems compared to RO system at ($P < 0.05$), and compared to AS system at ($P < 0.001$). MC and ML plots were significantly different in fungal communities' diversity at ($P < 0.001$). Higher diversity of total bacterial communities than total fungal communities was observed both at time zero and after cropping. We noticed the absence of significant differences in diversity due to N application on both total bacterial and fungal communities. This could be because amounts of total N (%) and total C (%) were moderate at time zero (0.22 and 2.39) respectively. Addition of mineral N to these soils may therefore not influence total diversity of microbial communities. This study was useful to get a better understanding on the impact of factors such as cropping systems, crop residue applications and N fertilization on total microbial diversity. The next step would be to investigate functional activities linked up with N cycle such as nitrification by using specific primers or quantitative PCR.

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